

WHAT IS CLAIMED IS:

1. An isolated polypeptide selected from the group consisting of:
 - (a) a polypeptide comprising at least 223 contiguous amino acids of an hPNQALRE protein selected from the group consisting of SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8;
 - (b) a polypeptide comprising an amino acid sequence that is at least 65% identical to amino acids 26-38 of SEQ ID NO:6;
 - (c) a polypeptide comprising an amino acid sequence identical to amino acids 26-38 of SEQ ID NO:6;
 - (d) a polypeptide comprising an amino acid sequence that is at least 65% identical to amino acids 181-201 of SEQ ID NO:6;
 - (e) a polypeptide comprising an amino acid sequence identical to amino acids 181-201 of SEQ ID NO:6; and
 - (f) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, and SEQ ID NO:8.
2. The isolated polypeptide of claim 1 comprising an amino acid sequence that is at least 65% identical to amino acids 26-38 of SEQ ID NO:6.
3. The isolated polypeptide of claim 1 comprising an amino acid sequence that is at least 65% identical to amino acids 181-201 of SEQ ID NO:6.
4. A fusion protein comprising a first protein segment and a second protein segment wherein said first protein segment is fused to said second protein segment by means of a peptide bond and wherein said first protein segment comprises an isolated polypeptide of claim 1.

5. A preparation of antibodies that specifically bind to an epitope defined in whole or in part by an isolated polypeptide of claim 1.

6. A cDNA molecule that encodes the isolated polypeptide of claim 1.

7. A cDNA molecule that encodes the isolated polypeptide of claim 2.

8. A cDNA molecule that encodes the isolated polypeptide of claim 3.

9. A cDNA molecule comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence that is at least 65% identical to nucleotides 76-114 of SEQ ID NO:5;

(b) a nucleotide sequence that is identical to nucleotides 76-114 of SEQ ID NO:5;

(c) a nucleotide sequence that is at least 65% identical to nucleotides 503-564 of SEQ ID NO:3 or to nucleotides 542-603 of SEQ ID NO:5;

(d) a nucleotide sequence that is identical to nucleotides 503-564 of SEQ ID NO:3 or to nucleotides 542-603 of SEQ ID NO:5; and

(e) a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7.

10. An isolated subgenomic polynucleotide or the complement thereof comprising a nucleotide sequence that hybridizes under stringent conditions to a

nucleotide sequence selected from the group consisting of nucleotides 76-114 of SEQ ID NO:5 and nucleotides 503-564 of SEQ ID NO:3.

11. A construct comprising:

a promoter; and

a polynucleotide segment comprising a cDNA of claim 6, wherein said polynucleotide segment is located downstream from said promoter and wherein transcription of said polynucleotide segment initiates at the promoter.

12. A construct comprising:

a promoter; and

a polynucleotide segment comprising a cDNA of claim 9, wherein said polynucleotide segment is located downstream from said promoter and wherein transcription of said polynucleotide segment initiates at the promoter.

13. A host cell comprising the construct of claim 11.

14. A host cell comprising the construct of claim 12.

15. A homologously recombinant cell having incorporated therein a new transcription initiation unit, wherein said new transcription initiation unit comprises:

(a) an exogenous regulatory sequence;

(b) an exogenous exon; and

(c) a splice donor site, wherein the new transcription initiation unit is located upstream of a coding sequence of a gene, wherein said gene has a coding sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID

NO:5 and SEQ ID NO:7 and wherein said exogenous regulatory sequence directs transcription of the coding sequence of the gene.

16. A method of diagnosing or prognosing neoplasia, comprising the step of comparing expression of a first *hPNQALRE* gene in a first tissue suspected of being neoplastic with expression of a second *hPNQALRE* gene in a second tissue which is normal, wherein said first and said second *hPNQALRE* genes comprise a coding sequence selected from the group consisting of:

- (a) SEQ ID NO:1;
- (b) SEQ ID NO:3;
- (c) SEQ ID NO:5;
- (d) SEQ ID NO:7;
- (e) nucleotides 76-114 of SEQ ID NO:5;
- (f) nucleotides 503-564 of SEQ ID NO:3; and
- (g) nucleotides 542-603 of SEQ ID NO:5, wherein over-expression of said first *hPNQALRE* gene in said first tissue indicates neoplasia in said first tissue.